Article

Benchmarking Summarization Methods for Scientific Abstracts: From Classical Models to LLMs

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Abstract

A single paragraph of about 200 words maximum. For research articles, abstracts should give a pertinent overview of the work. We strongly encourage authors to use the following style of structured abstracts, but without headings: (1) Background: place the question addressed in a broad context and highlight the purpose of the study; (2) Methods: describe briefly the main methods or treatments applied; (3) Results: summarize the article's main findings; (4) Conclusions: indicate the main conclusions or interpretations. The abstract should be an objective representation of the article, it must not contain results which are not presented and substantiated in the main text and should not exaggerate the main conclusions.

Keywords: benchmarking; natural language processing; text summarization; largue language models

1. Introduction

With the exponential growth of publicly available data, the effort to properly select relevant information has increased dramatically, leading to a scenario of information overloading in which important data may remain hidden. This has created a need for the development of reliable tools that can efficiently generate high-level summaries to highlight only the essential parts. Particularly, in the scientific field, where finding the right content is crucial for generation of novel hypothesis. To address this necessity, automatic text summarization (ATS) methods have undergone significant advances over time, enhancing their reliability in accurately summarizing relevant parts of complex research articles. While the history of ATS has been extensively evaluated and described by several articles [1,2], only few of them are tailored on scientific literature summarization [3,4]. This introduction, therefore, aims to cover all the methodological improvements in ATS, ranging from early statistical approaches to modern large language models (LLM), by linking each method to its scientific application.

1.1. Pre-Neural era: from word-frequency and early statistical methods to graph based approaches

Pre-neural era of summarization of scientific literature was characterized mainly by extractive approaches, where in an unsupervised way, summaries were generated by using word or concept frequency to identify relevant sentences. The first word-frequency based approaches were discussed by Luhn [5], who presented a method based on the assumption that recurrent words in a text are likely more important. Later, Edmunson [6]

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introduce concepts as cue words, title words, and sentence position to further enhance the automatic summarization process. Afterward, Term Frequency–Inverse Document Frequency (TF-IDF), was developed [7] and applied to text summarization by representing sentences as term-weight vectors that down-weight common biomedical terms and up-weight rare terms that might be of more relevance. Thus, word-frequency based approaches have been extensively adopted in scientific text summarization, being at the basis of more sophisticated strategies [8]. Lastly, graph-based methods were adopted, where sentences were represented as nodes and relations between sentences, calculated by using similarity measures (i.e cosine similarity of TF-IDF vectors), as edges. Two Graph-based methods gained popularity in the biomedicals domain: TextRank, that build a graph by breaking down the documents into single sentences and then exploit the PageRank algorithms to assign importance to each sentence, ultimately building the summary by using the top ranked ones [9,10] and LexRank that instead, use eigenvector centrality to find the ones that are most influential in the graph [11].

1.2. Neural network era: from sequence-to-sequence frameworks to modern LLM

With the advent of Sequence-to-Sequence (Seq2seq) frameworks, summaries were generated by paraphrasing and condensing text thanks to Encoder-Decoder architectures, originally implemented as Recurrent Neural Networks (RNNs), Long Short-Term Memory (LSTM) networks and Gated Recurrent Units (GRUs), which were applied in different domains such as the biomedical one [12,13]. Later, the introduction of self-attention mechanisms replaced recurrent networks, by processing sequences in parallel rather than sequentially, as a more effective method for capturing complex linguistic patterns and long context relationship [14]. This set the basis for transformer architectures that quickly gained popularity in performing a wide range of Natural Language Processing (NLP) tasks such as text summarization. One of the earliest and most influential transformer-based models, BERT, (Bidirectional Encoder Representations from Transformers) [15] was widely adopted in domain specific task thanks to the possibility to be fine-tuned by adding a task-specific output layer. Inspired by the BERT architecture, different models capable of performing abstractive summarization emerged: BART, Bidirectional and Auto-Regressive Transformer, is a denoising autoencoder for pretraining sequence-to-sequence models [16] that can be-trained or fine-tuned on scientific literature [17,18]. T5, Text-to-Text Transfer Transformer, was introduced as a unified text-to-text framework for a broad spectrum of NLP tasks due to its high flexibility with no need for architectural changes [19]. PEGASUS, Pre-training with Extracted Gap-sentences for Abstractive Summarization Sequence-to-sequence model, was proposed specifically for abstractive summarization tasks [20]. Notably, some PEGASUS versions tailored for scientific text summarization were developed such as "google/pegasus-pubmed" and "google/bigbird-pegasus-large-pubmed". RoBERTa, Robustly Optimized BERT Approach, is an improved version of BERT trained on a bigger corpus of text with some key optimizations, which leads to the creation of Longformer [21], a transformed based model, that with its Encoder-Decoder variant for text-to-text generation "allenai/led-base-16384" and "led-large-16384-arxiv" [22], can handle longer text. Despite these advances, the field of ATS quickly moved towards decoder-only architectures which are at the basis of LLMs, able to capture semantic relations with more flexibility and specificity. LLMs can be classified as general-purpose models, which leverage their broad domain knowledge for a variety of NLP tasks; reasoning-oriented models, characterized by a logical understanding of the text through iterative chain-of-thought processing and instruction tuning [23] and domain-specific ones, designed to address specific tasks. Over the years, several families of LLMs have been developed. From the first GPT-1 [24] to the recently released reasoning-oriented GPT-5 series (Nano, Mini, Full) and GPT:OSS, OpenAI GPT series models are all pre-trained using a huge amount of data in a self-supervised way. Similarly, Anthropic Claude Models are built on transformer architecture, trained through a Constitutional AI approach [25]. This family includes also a series of reasoning models such as Claude Sonnet-4, Opus-4 and Opus-4-1. Meta Llama family, where Llama 3 is the most capable model of the family up to now, comprises some domain-specific adaptations like OpenBioLLM-Llama-3, a variant of Meta's Llama-3 trained on a large corpus of high-quality biomedical data and medllama2, a medical language model built on Meta's LLaMA 2 architecture. Google and Microsoft developed a series of lightweight models such as Google Gemma series [26], with Gemma3 as its latest and most powerful reasoning model and the Microsoft Phi series, which comprises Phi-4-reasoning and Phi-4-mini-reasoning. Notably, Microsoft developed BioGPT [27], a model built on the GPT architecture and specifically fine-tuned on the biomedical domain. Other models such as Granite 4.0, a reasoning model of the IBM's Granite series and Magistral, the first reasoning model of the Mistral family have also been released. Remarkably, Mistral developed Biomistral, an open-source model pretrained on PubMed Central data. Moreover, Alibaba Cloud's introduced the Qwen 3 series as an open-source LLM family, where recently, SciLitLLM has been further developed as a specialized model for scientific literature understanding based on Qwen2.5 and trained through continual pre-training (CPT) and supervised fine-tuning (SFT) on scientific literature [28]. Lastly, DeepSeek has also developed some reinforcement learning (RL)-driven reasoning models, which are cost-effective and efficient [29]. Worth mentioning, APERTUS, Switzerland's first large-scale open, multilingual language model has been developed as an open-source model where the entire development process is openly accessible and fully documented.

At the best of our knowledge, no comprehensive peer-reviewed publications asses the efficiency of these methods for scientific text summarization. Therefore, in this manuscript, the performance of most of the discussed approaches is evaluated, aiming to highlight both strengths and limitations of each model to ultimately provide insights for accelerating knowledge discovery in molecular sciences.

2. Materials and Methods

2.1. Gold-Standard Dataset

To establish a reliable benchmark for automatic summarization, we assembled a gold-standard dataset of 1,000 biomedical articles drawn from a diverse set of peer-reviewed journals hosted on *ScienceDirect* and *Cell Press*. These journals were selected because, in addition to their focus on molecular and biomedical sciences, they provide a standardized *Highlights* section [30,31]. This section provides concise bullet points that capture the main findings of each article. These served as the reference summaries in our evaluation, while the corresponding abstracts were used as input texts for the summarization.

Articles were collected systematically across a variety of journals to ensure coverage of different fields within molecular sciences such as drug discovery, genomics, proteomics, biotechnology, and biochemistry. We selected 50 articles from each of the 20 journals, bringing the dataset to 1,000 in total. The distribution of articles across journals is summarized in Table 1.

Table 1. Overview of journals and number of articles included in the gold-standard dataset.

Publisher	Journal
ScienceDirect	Drug Discovery Today
ScienceDirect	Journal of Molecular Biology
ScienceDirect	FEBS Letters
ScienceDirect	Journal of Biotechnology
ScienceDirect	Gene
ScienceDirect	Genomics
ScienceDirect	Journal of Proteomics
ScienceDirect	The International Journal of Biochemistry & Cell Biology
ScienceDirect	Cytokine
ScienceDirect	Developmental Cell
Cell	Cell
Cell	Cancer Cell
Cell	Cell Chemical Biology
Cell	Cell Genomics
Cell	Cell Host & Microbe
Cell	Cell Metabolism
Cell	Cell Reports
Cell	Cell Reports Medicine
Cell	Cell Stem Cell
Cell	Cell Systems

This setup provides standardized pairs of abstracts and reference summaries that can be directly used for evaluating automatic summarization methods.

2.2. Summarization Methods

We evaluated 63 summarization models, ranging from simple frequency-based algorithms to state-of-the-art large language models (LLMs). By having this extensive coverage of models, we were able to compare established techniques with the latest transformer-based models under identical conditions.

The models were grouped into five categories:

1. Traditional models: As a foundation for comparison, we included two traditional extractive models: a simple frequency-based approach and TextRank [9]. These models provide a simple baseline to compare the more complex approaches with.
2. Encoder-Decoder models: We included a set of pre-trained encoder-decoder models, which are available through the HuggingFace library: BART (base and large) [16], T5 (base and large) [32], mT5 [33], and a variety of PEGASUS models [20]. These models are often applied for abstractive summarization and represent well-established neural systems within our benchmark.
3. General-purpose LLMs: We also evaluated a range of widely used large language models designed for broad application. This group includes models such as Gemma [26], Granite [34], LLaMA [35], Mistral [36], Phi [37,38], GPT [39,40], Claude [41], and Apertus [42], which represent the current landscape of general-purpose systems.
4. Reasoning-oriented LLMs: We further included several models developed with a focus on advanced reasoning capabilities. This group includes models from the DeepSeek-R1 family [43], Qwen [44], more GPT models such as GPT-oss [45] and GPT-5 [46], Magistral [47], and some additional Claude models. Their design emphasizes multi-step problem solving and allowed us to explore whether reasoning affects summarization performance.
5. Scientific/Biomedical models: To assess whether domain adaptation improves summarization quality, we included PEGASUS and BigBird models fine-tuned on PubMed

data (pegasus-pubmed & bigbird-pegasus-large-pubmed), LED [21] (arXiv-tuned), BioGPT [48], MedLLaMA2 [49], OpenBioLLM [50], BioMistral [51], and SciLitLLM1.5 models [52], which are trained on medical/biomedical data or on summarization tasks themselves.

The complete list of models included in each category is shown in Table 2.

Table 2. Overview of summarization methods/models evaluated in this study, organized by category.

Group	Methods/Models
Traditional models	textrank; frequency
Encoder-Decoder models	facebook/bart-base; facebook/bart-large-cnn; google-t5/t5-base; google-t5/t5-large; csebuetnlp/mT5_multilingual_XLSum; google/pegasus-xsum; google/pegasus-cnn_dailymail; google/pegasus-large
General-purpose LLMs	gemma3:270M; gemma3:1b; gemma3:4b; gemma3:12b; PetrosStav/gemma3-tools:4b; granite3.3:2b; granite3.3:8b; granite4:tiny-h; granite4:small-h; granite4:micro; granite4:micro-h; llama3.1:8b; llama3.2:1b; llama3.2:3b; mistral:7b; mistral-nemo:12b; mistral-small3.2:24b; mistral-small-2506; mistral-medium-2505; mistral-large-2411; mistral-medium-2508; phi3:3.8b; phi4:14b; gpt-3.5-turbo; gpt-4o; gpt-4o-mini; gpt-4.1; gpt-4.1-mini; claude-3-5-haiku-20241022; chat_swiss-ai/Apertus-8B-Instruct-2509
Reasoning-oriented LLMs	deepseek-r1:1.5b; deepseek-r1:7b; deepseek-r1:8b; deepseek-r1:14b; qwen3:4b; qwen3:8b; gpt-oss:20b; gpt-5-nano-2025-08-07; gpt-5-mini-2025-08-07; gpt-5-2025-08-07; claude-sonnet-4-20250514; claude-opus-4-20250514; claude-opus-4-1-20250805; magistral-medium-2509
Scientific/Biomedical models	google/pegasus-pubmed; google/bigbird-pegasus-large-pubmed; led_large_16384_arxiv_summarization; completion_microsoft/biogpt; medllama2:7b; chat_aaditya/OpenBioLLM-Llama3-8B; conversational_BioMistral/BioMistral-7B; chat_Uni-SMART/SciLitLLM1.5-7B; chat_Uni-SMART/SciLitLLM1.5-14B

With this selection, we covered models of different sizes and release periods, ensuring that both widely adopted systems and recent architectures were represented. Extraordinarily large models were not considered because their resource demands exceed what is practical for typical summarization pipelines and were beyond the resources available for this study.

These 63 diverse models were all tasked with generating summaries for each of the 1,000 abstracts in the dataset, resulting in 50,000 generated summaries available for evaluation.

2.3. Evaluation Metrics

As there is no single metric that can fully reflect summary quality, especially in the biomedical field where both coverage of key information and factual correctness are critical, we used a multitude of metrics grouped into three categories: traditional surface-level measures, embedding-based metrics, and performance-related measures that reflect the feasibility of using the methods in real-world applications. By combining all these metrics into one final overall score, we end up with a balanced benchmark value that reflects both summary quality and practical usability.

2.3.1. Surface-level Metrics

This group consists of metrics that compare the generated summaries with the reference summaries mainly at the word or phrase level. While they do not capture meaning beyond surface overlap, they remain common metrics in summarization research and provide a simple foundation for evaluation. We used three ROUGE variants (ROUGE-1, ROUGE-2, ROUGE-L) [53], BLEU [54], and METEOR [55]. ROUGE-1 and ROUGE-2 measure how many unigrams (single words) or bigrams (word pairs) from the reference appear in the generated output, while ROUGE-L identifies the longest sequence of words shared between the two. BLEU calculates how many n-grams in the output also occur in the reference, but it emphasizes precision rather than recall and applies a brevity penalty to counteract the tendency toward overly short summaries. METEOR extends n-gram matching by also considering word stems and synonyms, which makes it more tolerant to variations in wording. Together, these metrics offer a simple but transparent point of reference.

2.3.2. Embedding-based Metrics

To capture similarity beyond surface-level word overlap, we included a set of embedding-based metrics built on pre-trained transformer models. These methods generate vector representations of text, which allows them to capture similarity in meaning rather than just word overlap. We employed RoBERTa [56] and DeBERTa [57], two transformer-based models with strong performance across natural language processing tasks. In the context of summarization evaluation, they can be used to judge whether two summaries capture the same content even if phrased differently.

We also included all-mpnet-base-v2 [58], a transformer model fine-tuned for sentence similarity. Unlike RoBERTa and DeBERTa, which are primarily general-purpose encoders, MPNet was trained with a focus on aligning at the sentence-level. This focus makes it a useful complement to the other metrics, as it is particularly sensitive to whether the overall sense of a reference summary is preserved in the system output.

Finally, to evaluate factual consistency, we applied AlignScore [59], a metric designed to test whether the statements in a generated summary are supported by the source text. In contrast to the other metrics, we used AlignScore in a way where it does not compare the output to the reference summary but instead aligns it directly with the abstract, as factual accuracy can only be judged relative to the original input. This addition ensures that our evaluation is sensitive to errors and hallucinations that might otherwise be overlooked.

2.3.3. Performance Metrics

In addition to summary quality, we also considered practical aspects of model performance. Four measures were included: output token cost reflects the average length of generated summaries in tokens, as excessively long outputs increase runtime and resource requirements. Insufficient findings describe how often a model returned the predefined token 'INSUFFICIENT_FINDINGS' instead of producing a summary, capturing cases where it concluded the input did not contain substantive findings. Acceptance is the proportion of prompts for which a model produced an output, since some models occasionally failed to return a response. Finally, speed records the average time required to generate summaries, which is critical when processing large datasets.

These measures complement the quality metrics by addressing whether a method is not only accurate but also feasible to use in practice.

2.4. Benchmarking Framework

The benchmark was conducted using Python 3.12. Gold standard data were retrieved from open-access publications published by ScienceDirect and Cell Press through manual extraction of titles, abstracts, and highlight sections, along with metadata including publication URLs, identifiers, section types, and article types where available. All data were stored in machine-readable JSON format.

The framework was implemented using the Python standard library supplemented by several specialized packages: pandas [60] for data import and export, scikit-learn [61] for computing cosine similarities of embeddings and TF-IDF vectors, networkx [62] for graph construction and PageRank algorithm [63]. Additional evaluation metrics were computed using NLTK [64] for METEOR and BLEU scores, ROUGE-score, BERT-score [65], AlignScore, and sentence-transformers [66] with the all-mpnet-base-v2 model.

Communication with proprietary closed-source LLMs was facilitated through the official Python APIs provided by Anthropic, Mistral AI, and OpenAI. Local LLM execution was performed on a workstation equipped with a NVIDIA RTX A4000 GPU (16GB VRAM) running Ollama as a backend service, accessed through its Python API along with the transformers library [67].

All LLMs were configured with a temperature parameter of 0.2 to optimize reproducibility while avoiding completely deterministic outputs. For the latest generation of OpenAI models featuring adaptive reasoning capabilities, the configuration was set to `text.verbosity = low` and `reasoning.effort = minimal`. The full set of parameters and prompts are documented in the `config.py` file in the repository.

2.5. Data Availability

The complete source code, documentation, gold standard dataset, and processed results are available at:

https://www.github.com/Delta4AI/LLMTextSummarizationBenchmark.

3. Results

Our benchmark results offer a comparative view of summarization performance across all evaluated models. We first present overall rankings, followed by comparisons between the different model groups. Additionally, we examine results on individual metrics, runtime performance, and correlations between the evaluation metrics used.

3.1. Overall Model Performance

Figure 1 provides an overview of the performance of all evaluated models across all surface-level and embedding-based metrics. Each row corresponds to one model, and each column to a specific metric, with lower ranks indicating better performance. In addition to individual model names, the figure also indicates each model's family (e.g., GPT, DeepSeek, Gemma, Granite) and its broader category (e.g., encoder–decoder, general-purpose SLMs, reasoning-oriented LLMs). Models are sorted by their average rank across metrics. A hierarchical clustering based on Euclidean distance, which groups together models that exhibit similar ranking patterns across metrics, is shown on the right.

The best-performing models overall were from the Mistral family, with the top positions occupied by `ollama_mistral-small-3.2:24b`, `mistral_mistral-small-2506`, and `mistral_mistral_medium-2505`. Two OpenAI models (`gpt-5-nano-2025-08-07` and `gpt-5-mini-2025-08-07`) followed closely. These models achieved good ranks across nearly all surface-level metrics (ROUGE-1, ROUGE-2, ROUGE-L, METEOR, BLEU) and performed well on most embedding-based measures (RoBERTa, DeBERTa, all-mpnet-base-v2, AlignScore). Several other SLMs and LLMs also achieved competitive scores and maintained stable rankings across metrics.

At the lower end of the ranking, encoder–decoder architectures such as T5 and PEGASUS, traditional extractive models (TextRank and the frequency-based approach), and scientific/biomedical models such as MedLLaMA2 and BioGPT, achieved lower scores on most metrics.

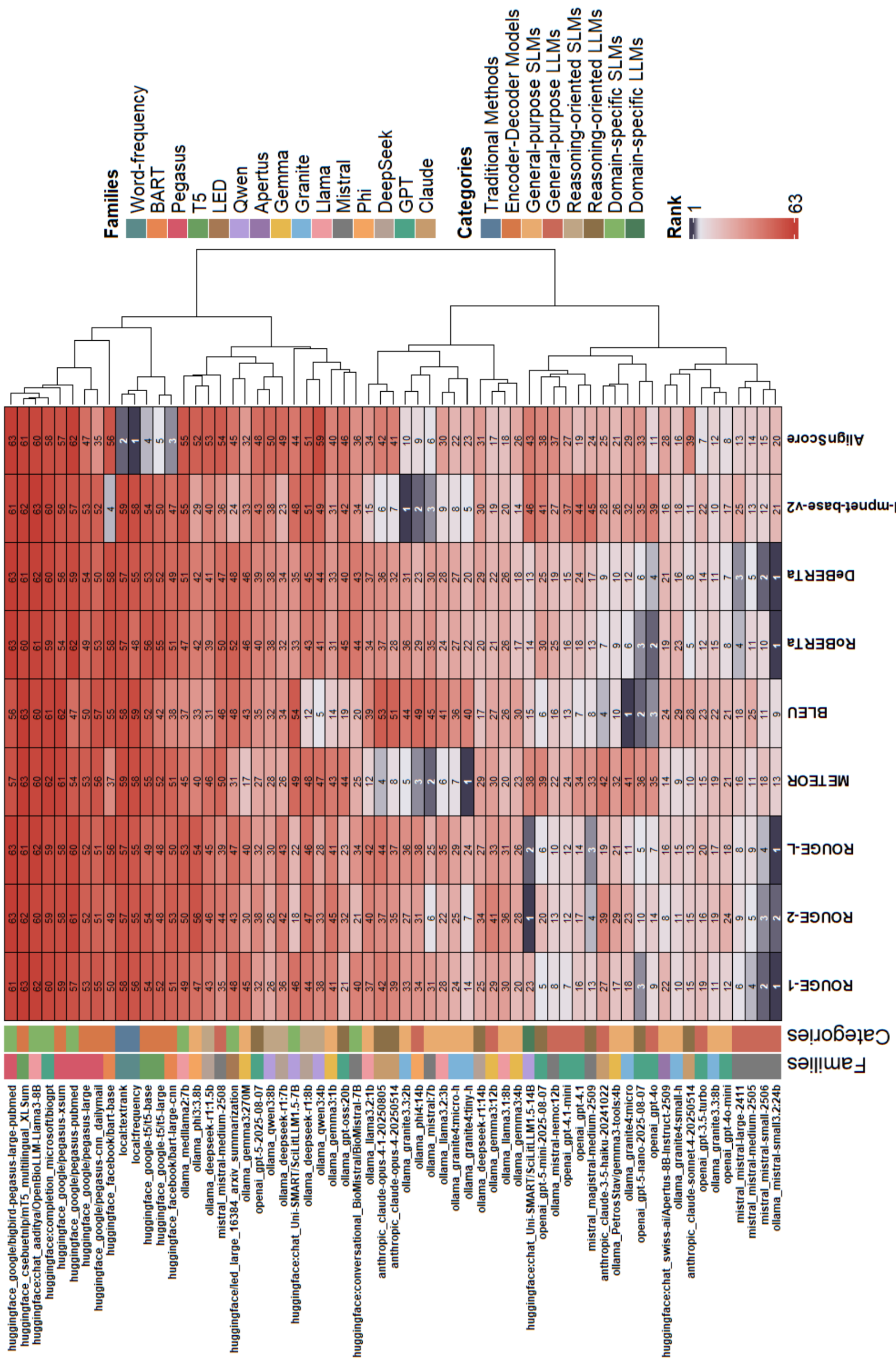


Figure 1. Model ranks across all surface-level and embedding-based metrics. Lower ranks indicate better performance. Models are ordered by their average rank and annotated with their family and category. The hierarchical clustering on the right groups models with similar ranking patterns.

3.2. Group Comparisons

Figure 2 summarizes the average performance of the eight model categories based on the overall Metric Mean Score. General-purpose LLMs achieved the highest mean score (0.523), followed closely by general-purpose SLMs (0.519) and reasoning-oriented LLMs

(0.515). Traditional extractive models and Encoder–decoder models performed considerably lower, with mean scores of 0.451 and 0.445, respectively. The Scientific/Biomedical SLMs showed the weakest overall performance (0.422), whereas the Scientific/Biomedical LLMs achieved a higher score (0.513; single model).

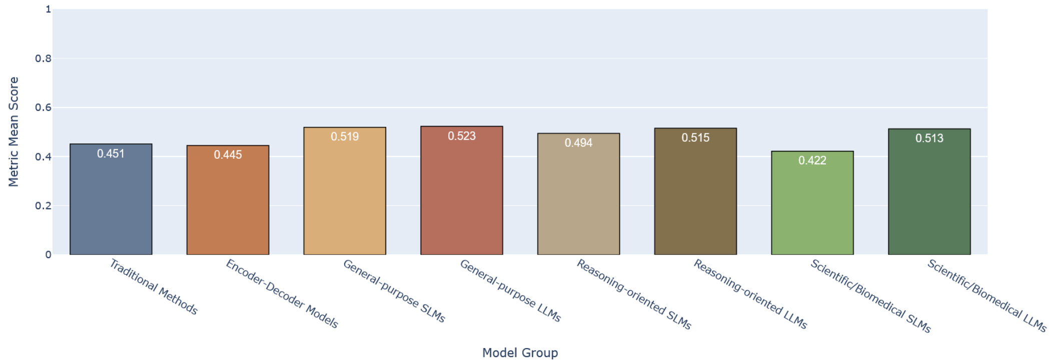
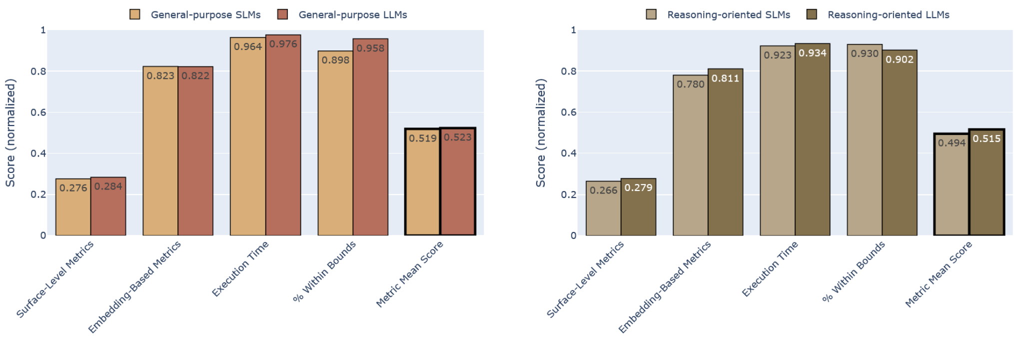


Figure 2. Average Metric Mean Score across the eight model categories. The figure highlights clear performance differences between categories, with general-purpose LLMs performing best overall, followed by general-purpose SLMs and reasoning-oriented LLMs. Traditional, encoder–decoder, and Scientific/Biomedical SLMs achieved notably lower scores.

3.2.1. SLMs vs. LLMs

To further analyze differences between small and large language models, we compared the performance of SLMs and LLMs within both the general-purpose and reasoning-oriented groups (Figure 3). In both categories, LLMs achieved slightly higher overall Metric Mean Scores and generally performed better on surface-level metrics. The results for embedding-based metrics were mixed, with general-purpose SLMs showing a small advantage over LLMs. Differences in execution time were minimal, while compliance with word-length bounds favored LLMs in the general-purpose group but SLMs in the reasoning-oriented group. The comparison for scientific/biomedical models is not shown here, as this category includes only a single LLM, which prevents a meaningful comparison.

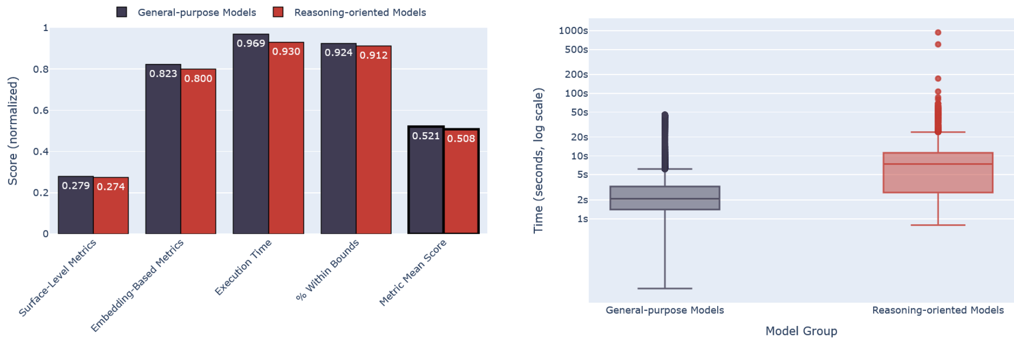


(**a**) General-purpose SLMs vs. LLMs. (**b**) Reasoning-oriented SLMs vs. LLMs.

Figure 3. (**a**) Comparison between general-purpose SLMs and LLMs across key evaluation metrics. (**b**) Comparison between reasoning-oriented SLMs and LLMs. In both groups, LLMs achieved slightly higher overall Metric Mean Scores, while SLMs occasionally performed better on individual metrics, particularly embedding-based or word-length compliance.

3.2.2. General-purpose Models vs. Reasoning-oriented Models

Figure 4a compares the two largest and most competitive groups—general-purpose and reasoning-oriented models—across multiple evaluation aspects. The comparison includes both SLMs and LLMs within each group. Overall, general-purpose models achieved slightly higher scores in all measured categories, including surface-level metrics, embedding-based metrics, execution time, compliance with word-length bounds, and overall Metric Mean Score. The largest difference was observed in execution time, where general-purpose models produced summaries more efficiently on average. Figure 4b provides a more detailed view of these runtime differences. The performance gap in quality metrics was smaller but consistent, with general-purpose models maintaining a slight advantage across both surface-level and embedding-based evaluations.



(**a**) General-purpose vs. reasoning-oriented models across key evaluation aspects.

(**b**) Execution time distribution for the same two groups.

Figure 4. (**a**) Comparison between general-purpose and reasoning-oriented models across key evaluation metrics. General-purpose models achieved higher scores across all categories, including surface-level and embedding-based metrics, execution time, compliance with word-length bounds, and overall Metric Mean Score. (**b**) Distribution of execution times for the same groups, showing that general-purpose models produced summaries more efficiently and with lower variability.

3.3. Metric Correlations

To examine how the different evaluation metrics relate to each other, we computed pairwise Pearson correlation coefficients across all models (Figure 5). Each cell in the matrix represents the correlation between two metrics based on their mean scores over all evaluated methods.

Strong positive correlations were observed among the surface-level metrics (ROUGE-1, ROUGE-2, ROUGE-L, METEOR, and BLEU). ROUGE variants were almost identical in their behavior ($\rho > 0.9$), while BLEU and METEOR showed slightly weaker but still substantial alignment with the ROUGE measures.

Most embedding-based metrics (RoBERTa, DeBERTa, and all-mpnet-base-v2) also showed very high internal consistency ($\rho > 0.8$), which reflects their shared focus on semantic similarity beyond surface-level overlap. When compared with the surface-level metrics, correlations were moderate to strong ($\rho \approx 0.7$–1.0), indicating that the two categories capture related but not identical dimensions of summary quality.

AlignScore correlated only moderately with the other metrics ($\rho \approx 0.4$–0.7), which can be attributed to its different point of reference, as it compares generated summaries directly with the source abstracts instead of the reference summaries used by the other metrics.

Overall, these relationships show that the various metrics are broadly consistent while still providing complementary perspectives. This supports the use of an aggregated "Metrics Mean Score" as a balanced indicator of overall summarization performance.

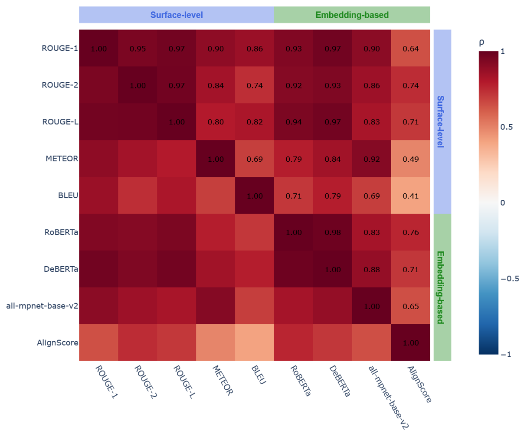


Figure 5. Correlation matrix of all evaluation metrics. Each cell represents the Pearson correlation coefficient (ρ) between two metrics based on their mean scores across models. Surface-level and most embedding-based metrics show strong internal consistency, while AlignScore exhibits lower correlations due to its distinct focus on factual consistency with the source abstracts.

3.4. Maybe include -> Performance by Metric Category

- show the performance when using only subsets of the metrics (only surface-level metrics vs only embedding-based metrics)

3.5. Maybe include -> Compliance with Summary Length

- not sure if this is worth its own subsection but it is interesting to see as it also gives a good feeling for how well a model follows the given instructions.

3.6. Maybe include -> Runtime Performance

- present the execution time across models, including distribution and outliers to give more context on execution time than just the average time for each model.

3.7. Maybe include -> Other things to possibly include

- maybe show a handpicked example of a good generated summary (good scores across all/most metrics, coming from a top-performing model) and a bad summary (bad scores across all/most metrics, coming from a low-performing model)

4. Discussion

4.1. Overview of Main Findings

The benchmarking analysis revealed clear performance differences between the evaluated summarization approaches. Overall, general-purpose large language models (LLMs) achieved the highest summarization quality across all surface-level and embedding-based metrics, followed closely by general-purpose small language models (SLMs) and reasoning-oriented LLMs. In contrast, domain-specific scientific/biomedical models, encoder–decoder architectures such as T5 and PEGASUS, and traditional extractive methods like TextRank all reached noticeably lower performance levels. These results highlight the clear progression from extractive and encoder–decoder approaches toward transformer-based models, while also showing that domain-specific fine-tuning alone does not necessarily lead to improved summarization quality.

4.2. Model Group Comparisons

To understand the causes of the observed performance differences, the models were compared by architecture, size, and domain focus. This analysis examines how model scale, reasoning ability, and domain specialization influence summarization quality in biomedical texts. The next sections discuss these aspects in detail by comparing large and small language models, general-purpose and scientific/biomedical models, and general-purpose and reasoning-oriented models.

4.2.1. Large vs. Small Language Models (LLMs vs. SLMs)

-discuss relationship between model size and summarization performance. https://arxiv.org/h

4.2.2. General-purpose vs. Scientific/Biomedical Models

-discuss why general-purpose models outperformed scientific/biomedical ones. https://arxiv.org/abs/2408.13833

4.2.3. General-purpose vs Reasoning-oriented Models

-discuss why reasoning-oriented models did not surpass general-purpose ones in summarization (primarily needs semantic compression and factual grounding rather than multi-step logical reasoning). https://arxiv.org/abs/2504.08120

4.3. Evaluation and Metric Considerations

-reflect how different evaluation metrics capture complementary aspects of summary quality. explain distinction between surface-level and embedding-based metrics. discuss observed correlations

4.4. Limitations and Future Work

-state main limitations (focus on single summarization task: abstract -> highlights, rapid evolution, absence of human quality evaluation)

4.5. Practical Implications and Applications

-emphasize how the results can guide model selection in biomedical NLP. highlight tradeoff between accuracy and efficiency. -conclude with short statement that general-purpose LLMs currently provide the most robust option for scientific summarization.

5. Conclusion

6. Results

This section may be divided by subheadings. It should provide a concise and precise description of the experimental results, their interpretation as well as the experimental conclusions that can be drawn.

6.1. Subsection

6.1.1. Subsubsection

Bulleted lists look like this:

- First bullet;
- Second bullet;
- Third bullet.

Numbered lists can be added as follows:

1. First item;
2. Second item;
3. Third item.

The text continues here.

6.2. Figures, Tables and Schemes

All figures and tables should be cited in the main text as Figure 6, Table 3, etc.

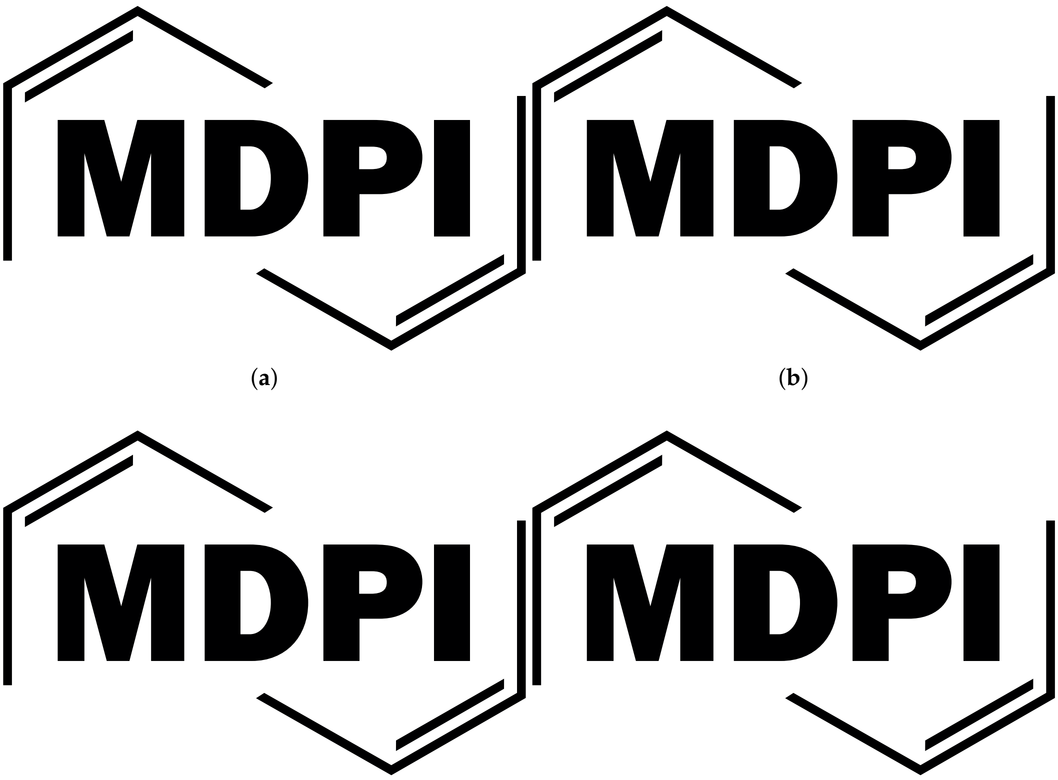
Figure 6. This is a figure. Schemes follow the same formatting.

Table 3. This is a table caption. Tables should be placed in the main text near to the first time they are cited.

Title 1	**Title 2**	**Title 3**
Entry 1	Data	Data
Entry 2	Data	Data [1]

[1] Tables may have a footer.

The text continues here (Figure 7 and Table 4).



(**a**) (**b**)

(**c**) (**d**)

Figure 7. This is a wide figure. Schemes follow the same formatting. If there are multiple panels, they should be listed as: (**a**) Description of what is contained in the first panel. (**b**) Description of what is contained in the second panel. (**c**) Description of what is contained in the third panel. (**d**) Description of what is contained in the fourth panel. Figures should be placed in the main text near to the first time they are cited. A caption on a single line should be centered.

Table 4. This is a wide table.

Title 1	Title 2	Title 3	Title 4
Entry 1 *	Data	Data	Data
	Data	Data	Data
	Data	Data	Data
Entry 2	Data	Data	Data
	Data	Data	Data
	Data	Data	Data

* Tables may have a footer.

Text.

Text.

6.3. Formatting of Mathematical Components

This is the example 1 of equation:

$$a = 1, \tag{1}$$

the text following an equation need not be a new paragraph. Please punctuate equations as regular text.

This is the example 2 of equation:

$$a = b + c + d + e + f + g + h + i + j + k + l + m + n + o + p + q + r + s + t + u + v + w + x + y + z \tag{2}$$

Please punctuate equations as regular text. Theorem-type environments (including propositions, lemmas, corollaries etc.) can be formatted as follows:

Theorem 1. *Example text of a theorem.*

The text continues here. Proofs must be formatted as follows:

Proof of Theorem 1. Text of the proof. Note that the phrase "of Theorem 1" is optional if it is clear which theorem is being referred to. □

The text continues here.

7. Discussion

Authors should discuss the results and how they can be interpreted from the perspective of previous studies and of the working hypotheses. The findings and their implications should be discussed in the broadest context possible. Future research directions may also be highlighted.

8. Conclusions

This section is not mandatory, but can be added to the manuscript if the discussion is unusually long or complex.

9. Patents

This section is not mandatory, but may be added if there are patents resulting from the work reported in this manuscript.

Author Contributions: For research articles with several authors, a short paragraph specifying their individual contributions must be provided. The following statements should be used "Conceptualization, X.X. and Y.Y.; methodology, X.X.; software, X.X.; validation, X.X., Y.Y. and Z.Z.; formal analysis, X.X.; investigation, X.X.; resources, X.X.; data curation, X.X.; writing—original draft preparation, X.X.; writing—review and editing, X.X.; visualization, X.X.; supervision, X.X.; project administration, X.X.; funding acquisition, Y.Y. All authors have read and agreed to the published version of the manuscript.", please turn to the CRediT taxonomy for the term explanation. Authorship must be limited to those who have contributed substantially to the work reported.

Funding: Please add: "This research received no external funding" or "This research was funded by NAME OF FUNDER grant number XXX." and and "The APC was funded by XXX". Check carefully that the details given are accurate and use the standard spelling of funding agency names at https://search.crossref.org/funding, any errors may affect your future funding.

Institutional Review Board Statement: In this section, you should add the Institutional Review Board Statement and approval number, if relevant to your study. You might choose to exclude this statement if the study did not require ethical approval. Please note that the Editorial Office might ask you for further information. Please add "The study was conducted in accordance with the Declaration of Helsinki, and approved by the Institutional Review Board (or Ethics Committee) of NAME OF INSTITUTE (protocol code XXX and date of approval)." for studies involving humans. OR "The animal study protocol was approved by the Institutional Review Board (or Ethics Committee) of NAME OF INSTITUTE (protocol code XXX and date of approval)." for studies involving animals. OR "Ethical review and approval were waived for this study due to REASON (please provide a detailed justification)." OR "Not applicable" for studies not involving humans or animals.

Informed Consent Statement: Any research article describing a study involving humans should contain this statement. Please add "Informed consent was obtained from all subjects involved in the study." OR "Patient consent was waived due to REASON (please provide a detailed justification)." OR "Not applicable" for studies not involving humans. You might also choose to exclude this statement if the study did not involve humans.

Written informed consent for publication must be obtained from participating patients who can be identified (including by the patients themselves). Please state "Written informed consent has been obtained from the patient(s) to publish this paper" if applicable.

Data Availability Statement: We encourage all authors of articles published in MDPI journals to share their research data. In this section, please provide details regarding where data supporting reported results can be found, including links to publicly archived datasets analyzed or generated during the study. Where no new data were created, or where data is unavailable due to privacy or ethical restrictions, a statement is still required. Suggested Data Availability Statements are available in section "MDPI Research Data Policies" at https://www.mdpi.com/ethics.

Acknowledgments: In this section you can acknowledge any support given which is not covered by the author contribution or funding sections. This may include administrative and technical support, or donations in kind (e.g., materials used for experiments). Where GenAI has been used for purposes such as generating text, data, or graphics, or for study design, data collection, analysis, or interpretation of data, please add "During the preparation of this manuscript/study, the author(s) used [tool name, version information] for the purposes of [description of use]. The authors have reviewed and edited the output and take full responsibility for the content of this publication."

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Abbreviations

The following abbreviations are used in this manuscript:

MDPI	Multidisciplinary Digital Publishing Institute
DOAJ	Directory of open access journals
TLA	Three letter acronym
LD	Linear dichroism

Appendix A

Appendix A.1

The appendix is an optional section that can contain details and data supplemental to the main text—for example, explanations of experimental details that would disrupt the flow of the main text but nonetheless remain crucial to understanding and reproducing the research shown; figures of replicates for experiments of which representative data are shown in the main text can be added here if brief, or as Supplementary Data. Mathematical proofs of results not central to the paper can be added as an appendix.

Table A1. This is a table caption.

Title 1	Title 2	Title 3
Entry 1	Data	Data
Entry 2	Data	Data

Appendix B

All appendix sections must be cited in the main text. In the appendices, Figures, Tables, etc. should be labeled, starting with "A"—e.g., Figure A1, Figure A2, etc.

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